

SEQ ID NO: 3

RESULT 5
AC004085/c
LOCUS AC004085 231758 bp DNA HTG 06-NOV-2000
DEFINITION Homo sapiens clone RP11-42B1, WORKING DRAFT SEQUENCE, 20 unordered
pieces.
ACCESSION AC004085
VERSION AC004085.6 GI:11079383
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 231758)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
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Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
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Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
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Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojebokan,I., Rolfe,M.,
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,
Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
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Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.
and Gibbs,R.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 231758)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (30-JAN-1998) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT On Nov 3, 2000 this sequence version replaced gi:9966929.
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Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: UG
Center clone name: RP11-42B1

----- Summary Statistics

Assembly program: Phrap; version 0.990329
Consensus quality: 224788 bases at least Q40
Consensus quality: 229074 bases at least Q30
Consensus quality: 230948 bases at least Q20
Estimated insert size: 227237; sum-of-contigs estimation
Estimated insert size: 317311; agarose-fp estimation
Quality coverage: 6.3x in Q20 bases; agarose-fp estimation
Quality coverage: 8.8x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
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*	81424	102538: contig of 21115 bp in length
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*	102639	119710: contig of 17072 bp in length
*	119711	119810: gap of unknown length
*	119811	136913: contig of 17103 bp in length
*	136914	137013: gap of unknown length
*	137014	153285: contig of 16272 bp in length
*	153286	153385: gap of unknown length
*	153386	167987: contig of 14602 bp in length
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*	168088	178731: contig of 10644 bp in length
*	178732	178831: gap of unknown length
*	178832	186641: contig of 7810 bp in length
*	186642	186741: gap of unknown length
*	186742	193215: contig of 6474 bp in length
*	193216	193315: gap of unknown length
*	193316	201310: contig of 7995 bp in length
*	201311	201410: gap of unknown length
*	201411	208647: contig of 7237 bp in length
*	208648	208747: gap of unknown length
*	208748	213802: contig of 5055 bp in length
*	213803	213902: gap of unknown length
*	213903	218049: contig of 4147 bp in length
*	218050	218149: gap of unknown length
*	218150	223316: contig of 5167 bp in length
*	223317	223416: gap of unknown length
*	223417	227389: contig of 3973 bp in length
*	227390	227489: gap of unknown length
*	227490	229032: contig of 1543 bp in length
*	229033	229132: gap of unknown length

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* 229133 230651: contig of 1519 bp in length
* 230652 230751: gap of unknown length
* 230752 231758: contig of 1007 bp in length.
FEATURES
    source          Location/Qualifiers
                        1. .231758
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="RP11-42B1"
BASE COUNT  64974 a 51086 c 51148 g 62641 t 1909 others
ORIGIN

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Query Match          100.0%; Score 31; DB 2; Length 231758;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ctcggcgggcctccccgccccttcgtcgtcc 31
        ||||||||||||||||||||||||||||
Db 89335 CTCGGCGGGCCTCCCCGCCCTTCGTCGTCC 89305

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SEQ ID NO: 6

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HTG 06-NOV-2000

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TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 231758)

AUTHORS Worley,K.C.

TITLE Direct Submission

JOURNAL Submitted (30-JAN-1998) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT On Nov 3, 2000 this sequence version replaced gi:9966929.

----- Genome Center

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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: UG
Center clone name: RP11-42B1
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Assembly program: Phrap; version 0.990329
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Consensus quality: 229074 bases at least Q30
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Estimated insert size: 317311; agarose-fp estimation
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Quality coverage: 8.8x in Q20 bases; sum-of-contigs estimation
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* 208648 208747: gap of unknown length
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* 218050 218149: gap of unknown length
* 218150 223316: contig of 5167 bp in length
* 223317 223416: gap of unknown length
* 223417 227389: contig of 3973 bp in length
* 227390 227489: gap of unknown length
* 227490 229032: contig of 1543 bp in length
* 229033 229132: gap of unknown length

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* 229133 230651: contig of 1519 bp in length
* 230652 230751: gap of unknown length
* 230752 231758: contig of 1007 bp in length.
FEATURES             Location/Qualifiers
  source              1..231758
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="RP11-42B1"
BASE COUNT      64974 a  51086 c  51148 g  62641 t   1909 others
ORIGIN

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Query Match      100.0%; Score 32; DB 2; Length 231758;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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SEQ ID NO: 9

RESULT 5

AC004085/c

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pieces.

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Gaps 0;

Qy 1 ccccttcggtcggtcctccttctccccct 27
|||||
Db 89318 CCCCTTCGTCGTCCTCCTTCTCCCCCT 89292

SEQ ID NO: 11

RESULT 3
AC004085/c
LOCUS AC004085 231758 bp DNA HTG 06-NOV-2000
DEFINITION Homo sapiens clone RP11-42B1, WORKING DRAFT SEQUENCE, 20 unordered pieces.
ACCESSION AC004085
VERSION AC004085.6 GI:11079383
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 231758)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsy,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,

Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
 Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
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 Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
 Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A.,
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 Thomas,N.,
 Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D.,
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 Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
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 Wooden,S.,
 Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S.,
 Nelson,D.
 and Gibbs,R.
 TITLE Direct Submission
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 231758)
 AUTHORS Worley,K.C.
 TITLE Direct Submission
 JOURNAL Submitted (30-JAN-1998) Molecular and Human Genetics, Baylor
 College of Medicine, One Baylor Plaza, Houston, TX 77030,
 USA
 COMMENT On Nov 3, 2000 this sequence version replaced gi:9966929.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: UG
 Center clone name: RP11-42B1
 ----- Summary Statistics
 Assembly program: Phrap; version 0.990329
 Consensus quality: 224788 bases at least Q40
 Consensus quality: 229074 bases at least Q30
 Consensus quality: 230948 bases at least Q20
 Estimated insert size: 227237; sum-of-contigs estimation
 Estimated insert size: 317311; agarose-fp estimation
 Quality coverage: 6.3x in Q20 bases; agarose-fp
 estimation
 Quality coverage: 8.8x in Q20 bases; sum-of-contigs
 estimation

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length      * NOTE: Estimated insert size may differ from sequence
            *
            * (see
http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 20 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *
            *      1      33241: contig of 33241 bp in length
            *      33242      33341: gap of unknown length
            *      33342      56391: contig of 23050 bp in length
            *      56392      56491: gap of unknown length
            *      56492      81323: contig of 24832 bp in length
            *      81324      81423: gap of unknown length
            *      81424      102538: contig of 21115 bp in length
            *      102539      102638: gap of unknown length
            *      102639      119710: contig of 17072 bp in length
            *      119711      119810: gap of unknown length
            *      119811      136913: contig of 17103 bp in length
            *      136914      137013: gap of unknown length
            *      137014      153285: contig of 16272 bp in length
            *      153286      153385: gap of unknown length
            *      153386      167987: contig of 14602 bp in length
            *      167988      168087: gap of unknown length
            *      168088      178731: contig of 10644 bp in length
            *      178732      178831: gap of unknown length
            *      178832      186641: contig of 7810 bp in length
            *      186642      186741: gap of unknown length
            *      186742      193215: contig of 6474 bp in length
            *      193216      193315: gap of unknown length
            *      193316      201310: contig of 7995 bp in length
            *      201311      201410: gap of unknown length
            *      201411      208647: contig of 7237 bp in length
            *      208648      208747: gap of unknown length
            *      208748      213802: contig of 5055 bp in length
            *      213803      213902: gap of unknown length
            *      213903      218049: contig of 4147 bp in length
            *      218050      218149: gap of unknown length
            *      218150      223316: contig of 5167 bp in length
            *      223317      223416: gap of unknown length
            *      223417      227389: contig of 3973 bp in length
            *      227390      227489: gap of unknown length
            *      227490      229032: contig of 1543 bp in length
            *      229033      229132: gap of unknown length
            *      229133      230651: contig of 1519 bp in length
            *      230652      230751: gap of unknown length
            *      230752      231758: contig of 1007 bp in length.

FEATURES             Location/Qualifiers
     source            1. .231758
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="RP11-42B1"

BASE COUNT      64974 a   51086 c   51148 g   62641 t   1909 others

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ORIGIN

Query Match 100.0%; Score 27; DB 2; Length 231758;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 27; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 1 cgctcggcgcccgcgcggtccccgcccgc 27
|||||
Db 89247 CGCTCGGCGCCCGCGCGTCCCCGCCGC 89221